

GenCore version 5.1.4\_db5-4578  
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## OM protein - protein search, using sw mode

Run On: March 25, 2003, 08:30:16 ; Search time 26 Seconds  
(without alignments)  
70,877 Million cell updates/sec

Title: US-09-982-259-7  
Perfect score: 72  
Sequence: 1 GMTFRAQECAFLTG 14

Scoring table: BLOSUM2  
Gapop 10.0 , Gapext 0.5

Searched: 611203 seqs, 131627836 residues

Total number of hits satisfying chosen parameters: 611203

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:  
1: /cgn2\_6/ptodata/2/paa/BCT\_NEW\_COMBO.pep:  
2: /cgn2\_6/ptodata/2/paa/US06\_NEWCOMB.pep:  
3: /cgn2\_6/ptodata/2/paa/US07\_NEWCOMB.pep:  
4: /cgn2\_6/ptodata/2/paa/US08\_NEWCOMB.pep:  
5: /cgn2\_6/ptodata/2/paa/US09\_NEWCOMB.pep:  
6: /cgn2\_6/ptodata/2/paa/US10\_NEWCOMB.pep:  
7: /cgn2\_6/ptodata/2/paa/US60\_NEWCOMB.pep:  
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Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	55.6	604	6 US-10-267-502-233	Sequence 233, App
2	39	54.2	494	6 US-10-282-122A-67089	Sequence 67089, A
3	38.5	53.5	629	6 US-10-282-122A-58229	Sequence 58229, A
4	37	51.4	244	6 US-10-369-493-16101	Sequence 16101, A
5	37	51.4	259	5 US-09-585-645A-66	Sequence 66, App
6	37	51.4	496	6 US-10-282-122A-55553	Sequence 55553, A
7	37	51.4	576	6 US-10-369-493-281	Sequence 281, App
8	37	51.4	602	6 US-10-126-122A-16	Sequence 16, App
9	36	50.0	246	5 US-09-134-000C-34-07	Sequence 3407, App
10	36	50.0	246	5 US-09-134-000C-34-07	Sequence 3407, App
11	36	50.0	267	6 US-10-282-122A-75641	Sequence 75641, A
12	36	50.0	362	5 US-09-134-000C-6004	Sequence 6004, App
13	36	50.0	362	5 US-09-134-000C-6004	Sequence 6004, App
14	36	50.0	375	5 US-09-134-000C-6005	Sequence 6005, App
15	36	50.0	375	5 US-09-134-000C-6005	Sequence 6005, App
16	36	50.0	498	6 US-10-282-122A-73008	Sequence 73008, A
17	36	50.0	500	6 US-10-282-122A-75641	Sequence 75641, A
18	36	50.0	554	1 PCT-US02-372727-10681	Sequence 10681, A
19	36	50.0	554	5 US-09-978-85-10681	Sequence 10681, A
20	36	50.0	554	6 US-10-057-498-10681	Sequence 10681, A
21	36	50.0	556	6 US-10-366-683-27601	Sequence 27601, A
22	36	50.0	561	6 US-10-259-194A-334	Sequence 334, App
23	36	50.0	4706	6 US-10-361-942-1281	Sequence 1281, App
24	35	48.6	237	6 US-10-369-493-17813	Sequence 17813, A
25	35	48.6	324	6 US-10-282-122A-55799	Sequence 55799, A
26	35	48.6	324	6 US-10-282-122A-59851	Sequence 59851, A

## ALIGNMENTS

RESULT 1  
US-10-267-502-233  
; Sequence 233, Application US/10267502

; GENERAL INFORMATION:  
; APPLICANT: Kim, Jaeseob  
; TITLE OF INVENTION: Obesity Linked Genes  
; FILE REFERENCE: LSD-074.16  
; CURRENT APPLICATION NUMBER: US/10/267,502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO: 233  
; LENGTH: 604  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-267-502-233

Query Match 1  
Best Local Similarity 55.6%;  
Matches 7; conservative 53.8%;  
; Score 40; DB 6;  
; Pred. No. 32; Mismatches 2; Indels 0; Gaps 0;  
; US-10-267-502-233

Query Match 2  
Best Local Similarity 55.6%;  
Matches 7; conservative 53.8%;  
; Score 40; DB 6;  
; Pred. No. 32; Mismatches 2; Indels 0; Gaps 0;  
; US-10-267-502-233

Query Match 3  
Best Local Similarity 55.6%;  
Matches 7; conservative 53.8%;  
; Score 40; DB 6;  
; Pred. No. 32; Mismatches 2; Indels 0; Gaps 0;  
; US-10-267-502-233

Query Match 4  
Best Local Similarity 55.6%;  
Matches 7; conservative 53.8%;  
; Score 40; DB 6;  
; Pred. No. 32; Mismatches 2; Indels 0; Gaps 0;  
; US-10-267-502-233

Query Match 5  
Best Local Similarity 55.6%;  
Matches 7; conservative 53.8%;  
; Score 40; DB 6;  
; Pred. No. 32; Mismatches 2; Indels 0; Gaps 0;  
; US-10-267-502-233

Query Match 6  
Best Local Similarity 55.6%;  
Matches 7; conservative 53.8%;  
; Score 40; DB 6;  
; Pred. No. 32; Mismatches 2; Indels 0; Gaps 0;  
; US-10-267-502-233

Query Match 7  
Best Local Similarity 55.6%;  
Matches 7; conservative 53.8%;  
; Score 40; DB 6;  
; Pred. No. 32; Mismatches 2; Indels 0; Gaps 0;  
; US-10-267-502-233

Query Match 8  
Best Local Similarity 55.6%;  
Matches 7; conservative 53.8%;  
; Score 40; DB 6;  
; Pred. No. 32; Mismatches 2; Indels 0; Gaps 0;  
; US-10-267-502-233

Query Match 9  
Best Local Similarity 55.6%;  
Matches 7; conservative 53.8%;  
; Score 40; DB 6;  
; Pred. No. 32; Mismatches 2; Indels 0; Gaps 0;  
; US-10-267-502-233

Query Match 10  
Best Local Similarity 55.6%;  
Matches 7; conservative 53.8%;  
; Score 40; DB 6;  
; Pred. No. 32; Mismatches 2; Indels 0; Gaps 0;  
; US-10-267-502-233

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; PRIOR APPLICATION NUMBER: 60/206, 848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207, 727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230, 335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230, 347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242, 578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253, 625
; PRIOR FILING DATE: 2000-11-77
; PRIOR APPLICATION NUMBER: 60/257, 931
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/267, 636
; PRIOR APPLICATION NUMBER: 60/269, 308
; PRIOR FILING DATE:
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 67089
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-10-282-122A-67089

Query Match 54.28%; Score 39; DB 6; Length 494;
Best Local Similarity 63.6%; Pred. No. 39;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.03A
CURRENT APPLICATION NUMBER: US-10/282,122A
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230, 347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1

RESULT 4
; SEQ ID NO: 143
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-282-122A-58229

Query Match 53.5%; Score 38.5; DB 6; Length 629;
Best Local Similarity 47.4%; Pred. No. 65;
Matches 9; Conservative 2; Mismatches 3; Indels 5; Gaps 1;
TITLE OF INVENTION: Compositions and Methods for Therapeutic Use of Atonal-association
FILE REFERENCE: P01899US2
CURRENT APPLICATION NUMBER: US-09/585,645A
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1

RESULT 5
; SEQ ID NO: 16601
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-369-493-16601

Query Match 51.4%; Score 37; DB 6; Length 244;
Best Local Similarity 35.7%; Pred. No. 43;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
TITLE OF INVENTION: for Deafness, Osteoarthritis, and Abnormal Cell Proliferation
FILE REFERENCE: P01899US2
CURRENT APPLICATION NUMBER: US-09/585,645A
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1

RESULT 6
; SEQ ID NO: 47374
; LENGTH: 244
; TYPE: PRT
; ORGANISM: C. elegans
US-10-369-493-47374

Query Match 51.4%; Score 37; DB 6; Length 244;
Best Local Similarity 35.7%; Pred. No. 43;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
TITLE OF INVENTION: for Deafness, Osteoarthritis, and Abnormal Cell Proliferation
FILE REFERENCE: P01899US2
CURRENT APPLICATION NUMBER: US-09/585,645A
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1

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RESULT 7  
 ; SEQ ID NO: 66  
 ; LENGTH: 259  
 ; TYPE: PRT  
 ; ORGANISM: FROG  
 ; SEQ ID NO: 66  
 US-09-585-645A-66  
 Query Match 51.4%; Score 37; DB 5; Length 259;  
 Best Local Similarity 53.3%; Pred. No. 46;  
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 MTFAQEGLTG 14  
 Db 211 LSFQFQEGLSG 223

RESULT 6  
 US-10-282-122A-55553  
 ; Sequence 55553, Application US/10282122A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Liangsu  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Malone, Cheryl  
 ; APPLICANT: Hasebeck, Robert  
 ; APPLICANT: Ohlsen, Kari  
 ; APPLICANT: Zyskind, Judith  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John  
 ; APPLICANT: Carr, Grant  
 ; APPLICANT: Yamamoto, Robert  
 ; APPLICANT: Forstth, R.  
 ; APPLICANT: Xu, H.  
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 ; FILE REFERENCE: E01TRA-03A  
 ; CURRENT APPLICATION NUMBER: US/10/282,122A  
 ; CURRENT FILING DATE: 2003-02-20  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/205,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/230,335  
 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: 60/230,347  
 ; PRIOR FILING DATE: 2000-09-09  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/267,636  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 78614  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 55553  
 ; LENGTH: 496  
 ; TYPE: PRT  
 ; ORGANISM: Enterobacter cloacae  
 US-10-282-122A-55553

Query Match 51.4%; Score 37; DB 6; Length 496;  
 Best Local Similarity 63.6%; Pred. No. 96;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Qy 4 FRAQEGLTG 14  
 Db 130 FRDQESEITG 140

RESULT 7  
 ; SEQ ID NO: 66  
 US-10-369-493-281  
 ; Sequence 281, Application US/10369493  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Chen, Xianlong  
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 ; PLANTS WITH IMPROVED PROPERTIES  
 ; FILE REFERENCE: 38-101520521B  
 ; CURRENT APPLICATION NUMBER: US/10/369,493  
 ; CURRENT FILING DATE: 2003-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/3160,039  
 ; PRIOR FILING DATE: 2002-02-21  
 ; NUMBER OF SEQ ID NOS: 47374  
 ; SEQ ID NO: 281  
 ; LENGTH: 576  
 ; TYPE: PRT  
 ; ORGANISM: Xenorhabdus nematophilus  
 US-10-369-493-281

Query Match 51.4%; Score 37; DB 6; Length 576;  
 Best Local Similarity 87.5%; Pred. No. 1.1e+02;  
 Matches 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 MTFRAGEG 9  
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 Db 569 MTFRAGEG 576

RESULT 8  
 US-10-126-052A-166  
 ; Sequence 166, Application US/10126052A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aziz, Natasha  
 ; APPLICANT: Murray, Richard  
 ; APPLICANT: Bios Biotechnology, Inc.  
 ; TITLE OF INVENTION: Methods of Diagnosis of Lung Cancer, Compositions and  
 ; Methods of Screening for Modulators of Lung Cancer  
 ; FILE REFERENCE: 018501-001540US  
 ; CURRENT APPLICATION NUMBER: US/10/126,052A  
 ; CURRENT FILING DATE: 2002-04-18  
 ; PRIOR APPLICATION NUMBER: US 60/784,770  
 ; PRIOR FILING DATE: 2001-04-18  
 ; PRIOR APPLICATION NUMBER: US 60/290,492  
 ; PRIOR FILING DATE: 2001-05-10  
 ; PRIOR APPLICATION NUMBER: US 60/339,245  
 ; PRIOR FILING DATE: 2001-11-09  
 ; PRIOR APPLICATION NUMBER: US 60/350,666  
 ; PRIOR FILING DATE: 2001-11-13  
 ; PRIOR APPLICATION NUMBER: US 60/334,370  
 ; PRIOR FILING DATE: 2001-11-29  
 ; PRIOR APPLICATION NUMBER: US 60/372,246  
 ; PRIOR FILING DATE: 2002-04-12  
 ; NUMBER OF SEQ ID NOS: 691  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 166  
 ; LENGTH: 602  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-126-052A-166

Query Match 51.4%; Score 37; DB 6; Length 602;  
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 FRAQEGLTG 13  
 :111111  
 Db 403 FRAKDGFSVT 412

RESULT 9  
US-09-134-000C-3407  
Sequence 3407, Application US/09134000C  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO  
FILE REFERENCE: 032796-032  
CURRENT APPLICATION NUMBER: US/09/134,000C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/055,778  
PRIOR FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 6812  
SOFTWARE: Patentin version 3.1  
SEQ ID NO: 3407  
LENGTH: 246  
TYPE: PRT  
ORGANISM: Enterococcus faecalis  
US-09-134-000C-3407

Query Match 50.0%; Score 36; DB 5; Length 246;  
Best Local Similarity 53.8%; Pred. No. 68;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
Db 1 MPPRGEEALLTG 13

Query 2 MTFRAQEGAFLTG 14  
Db 1 MPPRGEEALLTG 13

RESULT 10  
US-09-134-000C-3407  
Sequence 3407, Application US/09134000C  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO  
FILE REFERENCE: 032796-032  
CURRENT APPLICATION NUMBER: US/09/134,000C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/055,778  
NUMBER OF SEQ ID NOS: 6812  
SOFTWARE: Patentin version 3.1  
SEQ ID NO: 3407  
LENGTH: 246  
TYPE: PRT  
ORGANISM: Enterococcus faecalis  
US-09-134-000C-3407

Query Match 50.0%; Score 36; DB 5; Length 246;  
Best Local Similarity 53.8%; Pred. No. 68;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
Db 1 MPPRGEEALLTG 13

Query 2 MTFRAQEGAFLTG 14  
Db 1 MPPRGEEALLTG 13

RESULT 11  
US-10-282-1-122A-47803  
Sequence 47803, Application US/10282122A  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.

Query Match 50.0%; Score 36; DB 5; Length 362;  
Best Local Similarity 58.3%; Pred. No. 1e+02;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
Db 150 TFRDNESSYLAG 161

Query 3 TFRDNESSYLAG 14  
Db 150 TFRDNESSYLAG 161

RESULT 13



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